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TECH CENTER 1600/2900

P#7

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/543,371

DATE: 02/22/2001
 TIME: 12:14:29

Input Set : A:\14401027005.txt
 Output Set: N:\CRF3\02222001\I543371.raw

4 <110> APPLICANT: Raghuram Kalluri
 6 <120> TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS
 7 AND METHODS OF USE THEREOF
 10 <130> FILE REFERENCE: 1440.1027-005
 12 <140> CURRENT APPLICATION NUMBER: US 09/543,371
 13 <141> CURRENT FILING DATE: 2000-04-04
 15 <150> PRIOR APPLICATION NUMBER: US 09/335,224
 16 <151> PRIOR FILING DATE: 1999-06-17
 18 <150> PRIOR APPLICATION NUMBER: US 60/089,689
 19 <151> PRIOR FILING DATE: 1998-06-17
 21 <150> PRIOR APPLICATION NUMBER: US 60/126,175
 22 <151> PRIOR FILING DATE: 1999-03-25
 24 <160> NUMBER OF SEQ ID NOS: 18
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 690
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS /
 35 <222> LOCATION: (1)...(687)
 37 <400> SEQUENCE: 1
 38 tct gtt gat cac ggc ttc ctt gtg acc agg cat agt caa aca ata gat 48
 39 Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp
 40 1 5 10 15
 42 gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct 96
 43 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
 44 20 25 30
 46 ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc 144
 47 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
 48 35 40 45
 50 acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc 192
 51 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
 52 50 55 60
 54 tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg 240
 55 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
 56 65 70 75 80
 60 tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc 288
 61 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
 62 85 90 95
 64 acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag 336
 65 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
 66 100 105 110
 68 gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca 384
 69 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Glu Ile Pro
 70 115 120 125
 72 ccg tgc ccc agc ggg tgg tcc tgc ctg tgg atc ggc tac tot ttt gtg 432

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73 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val	
74 130 135 140	
76 atg cac acc agc gct ggt gca gaa ggc tct qgc caa gca gcc ctg gcg tcc	480
77 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser	
78 145 150 155 160	
80 ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag tgt	528
81 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys	
82 165 170 175	
84 cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg	576
85 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp	
86 180 185 190	
88 ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc	624
89 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser	
90 195 200 205	
92 acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa qtc	672
93 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val	
94 210 215 220	
96 tgt atg aga aga aca' taa	690
97 Cys Met Arg Arg Thr	
98 225	
101 <210> SEQ ID NO: 2	
102 <211> LENGTH: 229	
103 <212> TYPE: PRT	
104 <213> ORGANISM: Homo sapiens	
106 <400> SEQUENCE: 2	
107 Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp	
108 1 5 10 15	
109 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser	
110 20 25 30	
111 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly	
112 35 40 45	
113 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe	
114 50 55 60	
115 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser	
116 65 70 75 80	
117 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile	
118 85 90 95	
119 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu	
120 100 105 110	
121 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro	
122 115 120 125	
123 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val	
124 130 135 140	
125 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser	
126 145 150 155 160	
127 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys	
128 165 170 175	
129 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp	
130 180 185 190	

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131 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
132      195          200          205
133 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
134      210          215          220
135 Cys Met Arg Arg Thr
136 225
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 27
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for
146 Arresten
148 <400> SEQUENCE: 3
149 cgggatcctt ctgttgatca cggcttc
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 27
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: pET22b(+) reverse oligonucleotide primer for
158 Arresten
160 <400> SEQUENCE: 4
161 cccaaaggcttt gttcttctca tacagac
163 <210> SEQ ID NO: 5
164 <211> LENGTH: 684
165 <212> TYPE: DNA
166 <213> ORGANISM: Homo sapiens
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (1)...(681)
172 <400> SEQUENCE: 5
173 gtc agc atc ggc tac ctc ctg gtg aag cac agc cag acg gac cag gag
174 Val Ser Ile Gly Tyr Leu Leu Val Lys His Ser Gln Thr Asp Gln Glu
175 1      5          10          15
178 ccc atg tgc ccg gtg ggc atg aac aaa ctc tgg agt gga tac agc ctg
179 Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
180 20      25          30
182 ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg
183 Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
184 35      40          45
186 gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc
187 Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
188 50      55          60
190 aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac
191 Asn Pro Gly Asp Val Cys Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
192 65      70          75          80
194 tgg ctc tct acc act gcg ccc ctg ccc atg atg ccc gtg gcc gag gac
195 Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp

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196	85	90	95	
198	gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc			336
199	Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala			
200	100	105	110	
202	atc gcc atc qcg gtc cac agt cag gat gtG tcc atc cca cac tgc cca			384
203	Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro			
204	115	120	125	
206	gct ggg tgg cgg agt ttg tgg atc gga tat tcc ttc atg cac acg			432
207	Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr			
208	130	135	140	
210	gcg qcg gga gac gaa ggc ggt ggc caa tca ctg gtg tca ccg ggc			480
211	Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser			
212	145	150	155	160
214	tgt cta gag gac ttc cgc aca cca ttc atc gaa tgc aat gga ggc			528
215	Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly			
216	165	170	175	
218	cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc			576
219	Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr			
220	180	185	190	
222	acc att ccc gag cag agc ttc cag ggc tcg ccc tcc gcc gac acg ctc			624
223	Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu			
224	195	200	205	
226	aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg			672
227	Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met			
228	210	215	220	
230	aag aac ctg tga			684
231	Lys Asn Leu			
232	225			
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236	<211> LENGTH: 227			
237	<212> TYPE: PRT			
238	<213> ORGANISM: Homo sapiens			
240	<400> SEQUENCE: 6			
241	Val Ser Ile Gly Tyr Leu Leu Val Lys His Ser Gln Thr Asp Gln Glu			
242	1	5	10	15
243	Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu			
244	20	25	30	
245	Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu			
246	35	40	45	
247	Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys			
248	50	55	60	
249	Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr			
250	65	70	75	80
251	Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp			
252	85	90	95	
253	Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala			
254	100	105	110	
255	Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro			
256	115	120	125	

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257 Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
258 130 135 140
259 Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
260 145 150 155 160
261 Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
262 155 170 175
263 Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
264 180 185 190
265 Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
266 195 200 205
267 Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gin Val Cys Met
268 210 215 220
269 Lys Asn Leu
270 225
271 <210> SEQ ID NO: 7
272 <211> LENGTH: 27
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for
278 Canstatin
280 <400> SEQUENCE: 7
281 cgggatccctg tcagcatcgg ctacatc 27
283 <210> SEQ ID NO: 8
284 <211> LENGTH: 27
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: pET22b(+) reverse oligonucleotide primer for
290 Canstatin
292 <400> SEQUENCE: 8
293 cccaaggcttc aggtttttca tgcacac 27
295 <210> SEQ ID NO: 9
296 <211> LENGTH: 738
297 <212> TYPE: DNA
298 <213> ORGANISM: Homo sapiens
300 <220> FEATURE:
301 <221> NAME/KEY: CDS /
302 <222> LOCATION: (4)...(735)
304 <221> NAME/KEY: misc_feature
305 <222> LOCATION: (160)...(735)
306 <223> OTHER INFORMATION: Tumstatin N53
308 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (4)...(375)
310 <223> OTHER INFORMATION: Tumstatin 333
312 <221> NAME/KEY: misc_feature
313 <222> LOCATION: (376)...(735)
314 <223> OTHER INFORMATION: Tumstatin 334
316 <400> SEQUENCE: 9

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/543,371

DATE: 02/22/2001
TIME: 12:14:30

Input Set : A:\14401027005.txt
Output Set: N:\CRF3\02222001\1543371.raw